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## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

- (i) APPLICANT: STRACKE, MARY; LIOTTA, LANCE;  
SCHIFFMANN, ELLIOTT; KRUTZSCH,  
HENRY
- (ii) TITLE OF INVENTION: MOTILITY STIMULATING  
PROTEIN USEFUL IN CANCER DIAGNOSIS AND  
THERAPY
- (iii) NUMBER OF SEQUENCES: 54
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: MORGAN & FINNEGAN
  - (B) STREET: 345 PARK AVENUE
  - (C) CITY: NEW YORK
  - (D) STATE: NEW YORK
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy Disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: WordPerfect 5.1
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 25-MAY-1994
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
  - (A) APPLICATION NUMBER: 07/822,043
  - (B) FILING DATE: 17-JAN-1992
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: DOROTHY R. AUTH
  - (B) REGISTRATION NUMBER: 36,434
  - (C) DOCKET NUMBER: 2026-4149US1
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (212) 758-4800
  - (B) TELEFAX: (212) 751-6849

### (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5
  - (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp His Val Ala Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Leu Asp Val Tyr Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Tyr Pro Ala Phe Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln Ala Glu Val Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Pro Glu Glu Val Thr Arg Pro Asn Tyr Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Tyr Asp Val Pro Trp Asn Glu Thr Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Val Pro Pro Phe Glu Asn Ile Glu Leu Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Gly Gln Pro Leu Trp Ile Thr Ala Thr Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Asn Ser Met Gln Thr Val Phe Val Gly Tyr Gly  
1 5 10  
Pro Thr Phe Lys  
15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp Ile Glu His Leu Thr Ser Leu Asp Phe Phe Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val Asp  
1 5 10  
Asp Ile Thr Leu Val Pro Glu Thr Leu Gly Arg  
15 20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTGGCAGCN ACRTGCCA

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(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGGCAYGTNG CTGCCAAC

18

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTTGAAGGCA GGGTA

15

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAYCCTGCNT TYAAG

15

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTNACYTCY TCAGG

15

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCTGARGARG TNACC

15

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

NGTNGCRTCR AATGGCACRT C'

21

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAYGTGCCAT TYGAYGCNAC N

21

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTTDATRTTS TCRAATGGGG G

21

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCCCCATTTG AGAACATCAA C

21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTTNGTNGCN GTDATCCANA RGGGYTGGCC GCC

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(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCGGCCARC CCYTNTGGAT HACNGCNACN AAG

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(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTTRAAGGTG GGGCCRTAGC CCACRAAGAC TGTYTGCAT

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(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGCARACAG TCTTYGTGGG CTAYGGCCCC ACCTTYAAR

39

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gln Tyr Leu His Gln Tyr Gly Ser Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Val Leu Asn Tyr Phe  
1 5



(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Tyr Leu Asn Ala Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

His Leu Leu Tyr Gly Arg Pro Ala Val Leu Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Tyr Pro Glu Ile Leu Thr Pro Ala Asp Asn  
1 5 10

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Xaa Tyr Gly Phe Leu Phe Pro Pro Tyr Leu Ser Ser Ser  
1 5 10  
Pro

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Thr Phe Pro Asn Leu Tyr Thr Phe Ala Thr Gly Leu  
1 5 10  
Tyr

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val Asn Val Ile Ser Gly Pro Ile Asp Asp Tyr Asp  
1 5 10  
Tyr Asp Gly Leu His Asp Thr Glu Asp Lys  
15 20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE: Melanoma
- (H) CELL LINE: A2058
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Putative protein sequence of A2058 Autotaxin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Cys	His	Asp	Phe	Asp	Glu	Leu	Cys	Leu	Lys	Thr	Ala	Arg	Gly	Trp	Glu	5	10	15
Cys	Thr	Lys	Asp	Arg	Cys	Gly	Glu	Val	Arg	Asn	Glu	Glu	Asn	Ala	Cys	20	25	30
His	Cys	Ser	Glu	Asp	Cys	Leu	Ala	Arg	Gly	Asp	Cys	Cys	Thr	Asn	Tyr	35	40	45
Gln	Val	Val	Cys	Lys	Gly	Glu	Ser	His	Trp	Val	Asp	Asp	Asp	Cys	Glu	50	55	60
Glu	Ile	Lys	Ala	Ala	Glu	Cys	Pro	Ala	Gly	Phe	Val	Arg	Pro	Pro	Leu	65	70	75
Ile	Ile	Phe	Ser	Val	Asp	Gly	Phe	Arg	Ala	Ser	Tyr	Met	Lys	Lys	Gly	85	90	95
Ser	Lys	Val	Met	Pro	Asn	Ile	Glu	Lys	Leu	Arg	Ser	Cys	Gly	Thr	His	100	105	110
Ser	Pro	Tyr	Met	Arg	Pro	Val	Tyr	Pro	Thr	Lys	Thr	Phe	Pro	Asn	Leu	115	120	125
Tyr	Thr	Leu	Ala	Thr	Gly	Leu	Tyr	Pro	Glu	Ser	His	Gly	Ile	Val	Gly	130	135	140
Asn	Ser	Met	Tyr	Asp	Pro	Val	Phe	Asp	Ala	Thr	Phe	His	Leu	Arg	Gly	145	150	155
Arg	Glu	Lys	Phe	Asn	His	Arg	Trp	Trp	Gly	Gly	Gln	Pro	Leu	Trp	Ile	165	170	175
Thr	Ala	Thr	Lys	Gln	Gly	Val	Lys	Ala	Gly	Thr	Phe	Phe	Trp	Ser	Val	180	185	190
Val	Ile	Pro	His	Glu	Arg	Arg	Ile	Leu	Thr	Ile	Leu	Arg	Trp	Leu	Thr	195	200	205
Leu	Pro	Asp	His	Glu	Arg	Pro	Ser	Val	Tyr	Ala	Phe	Tyr	Ser	Glu	Gln	210	215	220

Pro	Asp	Phe	Ser	Gly	His	Lys	Tyr	Gly	Pro	Phe	Gly	Pro	Glu	Glu	Ser
225					230					235					240
Ser	Tyr	Gly	Ser	Pro	Phe	Thr	Pro	Ala	Lys	Arg	Pro	Lys	Arg	Lys	Val
				245					250					255	
Ala	Pro	Lys	Arg	Arg	Gln	Glu	Arg	Pro	Val	Ala	Pro	Pro	Lys	Lys	Arg
			260					265					270		
Arg	Arg	Lys	Ile	His	Arg	Met	Asp	His	Tyr	Ala	Ala	Glu	Thr	Arg	Gln
		275					280					285			
Asp	Lys	Met	Thr	Asn	Pro	Leu	Arg	Glu	Ile	Asp	Lys	Ile	Val	Gly	Gln
	290					295					300				
Leu	Met	Asp	Gly	Leu	Lys	Gln	Leu	Lys	Leu	Arg	Arg	Cys	Val	Asn	Val
305					310					315					320
Ile	Phe	Val	Gly	Asp	His	Gly	Met	Glu	Asp	Val	Thr	Cys	Asp	Arg	Thr
			325						330					335	
Glu	Phe	Leu	Ser	Asn	Tyr	Leu	Thr	Asn	Val	Asp	Asp	Ile	Thr	Leu	Val
			340					345					350		
Pro	Gly	Thr	Leu	Gly	Arg	Ile	Arg	Ser	Lys	Phe	Ser	Asn	Asn	Ala	Lys
		355					360					365			
Tyr	Asp	Pro	Lys	Ala	Ile	Ile	Ala	Asn	Leu	Thr	Cys	Lys	Lys	Pro	Asp
	370					375					380				
Gln	His	Phe	Lys	Pro	Tyr	Leu	Lys	Gln	His	Leu	Pro	Lys	Arg	Leu	His
385					390					395					400
Tyr	Ala	Asn	Asn	Arg	Arg	Ile	Glu	Asp	Ile	His	Leu	Leu	Val	Glu	Arg
				405				410						415	
Arg	Trp	His	Val	Ala	Arg	Lys	Pro	Leu	Asp	Val	Tyr	Lys	Lys	Pro	Ser
			420					425					430		
Gly	Lys	Cys	Phe	Phe	Gln	Gly	Asp	His	Gly	Phe	Asp	Asn	Lys	Val	Asn
		435					440					445			
Ser	Met	Gln	Thr	Val	Phe	Val	Gly	Tyr	Gly	Pro	Thr	Phe	Lys	Tyr	Lys
	450					455					460				
Thr	Lys	Val	Pro	Pro	Phe	Glu	Asn	Ile	Glu	Leu	Tyr	Asn	Val	Met	Cys
465					470					475					480
Asp	Leu	Leu	Gly	Leu	Lys	Pro	Ala	Pro	Asn	Asn	Gly	Thr	His	Gly	Ser
				485					490					495	
Leu	Asn	His	Leu	Leu	Arg	Thr	Asn	Thr	Phe	Arg	Pro	Thr	Met	Pro	Glu
			500					505					510		
Glu	Val	Thr	Arg	Pro	Asn	Tyr	Pro	Gly	Ile	Met	Tyr	Leu	Gln	Ser	Asp
		515					520					525			
Asp	Asp	Leu	Gly	Cys	Thr	Cys	Asp	Asp	Lys	Val	Glu	Pro	Lys	Asn	Lys
	530					535					540				
Leu	Asp	Glu	Leu	Asn	Lys	Arg	Leu	His	Thr	Lys	Gly	Ser	Thr	Glu	Glu
545					550					555					560
Arg	His	Leu	Leu	Tyr	Gly	Arg	Pro	Ala	Val	Leu	Tyr	Arg	Thr	Arg	Tyr
				565					570					575	
Asp	Ile	Leu	Tyr	His	Thr	Asp	Phe	Glu	Ser	Gly	Tyr	Ser	Glu	Ile	Phe
			580					585					590		
Leu	Met	Leu	Leu	Trp	Thr	Ser	Tyr	Thr	Val	Ser	Lys	Gln	Ala	Glu	Val
		595					600					605			
Ser	Ser	Val	Pro	Asp	His	Leu	Thr	Ser	Cys	Val	Arg	Pro	Asp	Val	Arg
	610					615					620				
Val	Ser	Pro	Ser	Phe	Ser	Gln	Asn	Cys	Leu	Ala	Tyr	Lys	Asn	Asp	Lys
625					630					635					640

Gln	Met	Ser	Tyr	Gly	Phe	Leu	Phe	Pro	Pro	Tyr	Leu	Ser	Ser	Ser	Pro
				645					650					655	
Glu	Ala	Lys	Tyr	Asp	Ala	Phe	Leu	Val	Thr	Asn	Met	Val	Pro	Met	Tyr
			660					665					670		
Pro	Ala	Phe	Lys	Arg	Val	Trp	Asn	Tyr	Phe	Gln	Arg	Val	Leu	Val	Lys
		675					680					685			
Lys	Tyr	Ala	Ser	Glu	Arg	Asn	Gly	Val	Asn	Val	Ile	Ser	Gly	Pro	Ile
	690					695					700				
Phe	Asp	Tyr	Asp	Tyr	Asp	Gly	Leu	His	Asp	Thr	Glu	Asp	Lys	Ile	Lys
705				710						715					720
Gln	Tyr	Val	Glu	Gly	Ser	Ser	Ile	Pro	Val	Pro	Thr	His	Tyr	Tyr	Ser
			725						730					735	
Ile	Ile	Thr	Ser	Cys	Leu	Asp	Phe	Thr	Gln	Pro	Ala	Asp	Lys	Cys	Asp
			740					745					750		
Gly	Pro	Leu	Ser	Val	Ser	Ser	Phe	Ile	Leu	Pro	His	Arg	Pro	Asp	Asn
		755					760					765			
Glu	Glu	Ser	Cys	Asn	Ser	Ser	Glu	Asp	Glu	Ser	Lys	Trp	Val	Glu	Glu
	770					775					780				
Leu	Met	Lys	Met	His	Thr	Ala	Arg	Val	Arg	Asp	Ile	Glu	His	Leu	Thr
785				790						795					800
Ser	Leu	Asp	Phe	Phe	Arg	Lys	Thr	Ser	Arg	Ser	Tyr	Pro	Glu	Ile	Leu
			805						810					815	
Thr	Leu	Lys	Thr	Tyr	Leu	His	Thr	Tyr	Glu	Ser	Glu	Ile			
			820					825							

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2946
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE: Melanoma
  - (H) CELL LINE: A2058
  - (I) ORGANELLE:
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Partial DNA Sequence of  
A2058 Autotaxin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCTGCCATGA	CTTTGATGAG	CTGTGTTTGA	AGACAGCCCCG	TGGCTGGGAG	TGTACTAAGG	60
ACAGATGTGG	AGAAGTCAGA	AATGAAGAAA	ATGCCTGTCA	CTGCTCAGAG	GACTGCTTGG	120
CCAGGGGAGA	CTGCTGTACC	AATTACCAAG	TGGTTTGCAA	AGGAGAGTCG	CATTGGGTTG	180
ATGATGACTG	TGAGGAAATA	AAGGCCGCAG	AATGCCCTGC	AGGGTTTGT	CGCCCTCCAT	240
TAATCATCTT	CTCCGTGGAT	GGCTTCCGTG	CATCATACT	GAAGAAAGGC	AGCAAAGTCA	300
TGCCTAATAT	TGAAAAACTA	AGGTCTTGTG	GCACACACTC	TCCCTACATG	AGGCCGGTGT	360
ACCCAACATA	AACCTTTCCT	AACCTTATACA	CTTTGGCCAC	TGGGCTATAT	CCAGAATCAC	420
ATGGAATTGT	TGGCAATTCA	ATGTATGATC	CTGTATTTGA	TGCCACTTTT	CATCTGCGAG	480
GGCGAGAGAA	ATTTAATCAT	AGATGGTGGG	GAGGTCAACC	GCTATGGATT	ACAGCCACCA	540
AGCAAGGGGT	GAAAGCTGGA	ACATTCTTTT	GGTCTGTTGT	CATCCCTCAC	GAGCGGAGAA	600
TATTAACCAT	ATTGCGGTGG	CTCACCTTGC	CAGATCATGA	GAGGCCTTCG	GTCTATGCCT	660
TCTATTCTGA	GCAACCTGAT	TTCTCTGGAC	ACAAATATGG	CCCTTTCGGC	CCTGAGGAGA	720
GTAGTTATGG	CTCACCTTTT	ACTCCGGCTA	AGAGACCTAA	GAGGAAAGTT	GCCCCTAAGA	780
GGAGACAGGA	AAGACCAGTT	GCTCCTCCAA	AGAAAAGAAG	AAGAAAAATA	CATAGGATGG	840
ATCATTATGC	TGCGGAAACT	CGTCAGGACA	AAATGACAAA	TCCTCTGAGG	GAAATCGACA	900
AAATTGTGGG	GCAATTAATG	GATGGACTGA	AACAACATAA	ACTGCGTCGG	TGTGTCAACG	960
TCATCTTTGT	CGGAGACCAT	GGAATGGAAG	ATGTCACATG	TGATAGAACT	GAGTTCTTGA	1020
GTAATTACCT	AACTAATGTG	GATGATATTA	CTTTAGTGCC	TGGAACCTCTA	GGAAGAATTC	1080
GATCCAAATT	TAGCAACAAT	GCTAAATATG	ACCCCAAAGC	CATTATTGCC	AATCTCACGT	1140
GTAAAAAACC	AGATCAGCAC	TTTAAGCCTT	ACTTGAAACA	GCACCTTCCC	AAACGTTTGC	1200
ACTATGCCAA	CAACAGAAGA	ATTGAGGATA	TCCATTTATT	GGTGGAACGC	AGATGGCATG	1260
TTGCAAGGAA	ACCTTTGGAT	GTTTATAAGA	AACCATCAGG	AAAATGCTTT	TTCCAGGGAG	1320
ACCACGGATT	TGATAACAAG	GTCAACAGCA	TGCAGACTGT	TTTTGTAGGT	TATGGCCCAA	1380
CATTTAAGTA	CAAGACTAAA	GTGCCTCCAT	TTGAAAACAT	TGAACCTTAC	AATGTTATGT	1440
GTGATCTCCT	GGGATTGAAG	CCAGCTCCTA	ATAATGGGAC	CCATGGAAGT	TTGAATCATC	1500
TCCTGCGCAC	TAATACCTTC	AGGCCAACCA	TGCCAGAGGA	AGTTACCAGA	CCCAATTATC	1560
CAGGGATTAT	GTACCTTCAG	TCTGATTTTG	ACCTGGGCTG	CACTTGTGAT	GATAAGGTAG	1620
AGCCAAAGAA	CAAGTTGGAT	GAACCTCAACA	AACGGCTTCA	TACAAAAGGG	TCTACAGAAG	1680
AGAGACACCT	CCTCTATGGG	CGACCTGCAG	TGCTTTATCG	GACTAGATAT	GATATCTTAT	1740
ATCACACTGA	CTTTGAAAGT	GGTTATAGTG	AAATATTCTT	AATGCTACTC	TGGACATCAT	1800
ATACTGTTTC	CAAACAGGCT	GAGGTTTCCA	GCGTTCTTGA	CCATCTGACC	AGTTGCGTCC	1860
GGCCTGATGT	CCGTGTTTCT	CCGAGTTTCA	GTCAGAACTG	TTTGGCCTAC	AAAAATGATA	1920
AGCAGATGTC	CTACGGATTG	CTCTTTCCTC	CTTATCTGAG	CTCTTCACCA	GAGGCTAAAT	1980
ATGATGCATT	CCTTGTAACC	AATATGGTTC	CAATGTATCC	TGCTTTCAAA	CGGGTCTGGA	2040
ATTATTTCCA	AAGGGTATTG	GTGAAGAAAT	ATGCTTCGGA	AAGAAATGGA	GTTAACGTGA	2100
TAAGTGGACC	AATCTTCGAC	TATGACTATG	ATGGCTTACA	TGACACAGAA	GACAAAATAA	2160
AACAGTACGT	GGAAGGCAGT	TCCATTCTCT	TTCCAACCTCA	CTACTACAGC	ATCATCACCA	2220
GCTGTCTGGA	TTTCACTCAG	CCTGCCGACA	AGTGTGACGG	CCCTCTCTCT	GTGTCTCTCT	2280
TCATCCTGCC	TCACCGGCCT	GACAAAGAGG	AGAGCTGCAA	TAGCTCAGAG	GACGAATCAA	2340
AATGGGTTAG	AGAAGTCATG	AAGATGCACA	CAGCTAGGGT	GCGTGACATT	GAACATCTCA	2400
CCAGCCTGGA	CTTCTTCCGA	AAGACCAGCC	GCAGCTACCC	AGAAATCCTG	ACACTCAAGA	2460
CATACCTGCA	TACATATGAG	AGCGAGATTT	AACTTTCTGA	GCATCTGCAG	TACAGTCTTA	2520
TCAAACGGTT	GTATATTTTT	ATATTGTTTT	TGTATTTATT	AATTTGAAAC	CAGGACATTA	2580
AAAATGTTAG	TATTTTAATC	CTGTACCAAA	TCTGACATAT	TATGCCGTGAA	TGACTCCACT	2640
GTTTTTCTCT	AATGCTTGAT	TTAGGTAGCC	TTGTGTTCTG	AGTAGAGCTT	GTAATAAATA	2700
CTGCAGCTTG	AGAAAAAGTG	GAAGCTTCTA	AATGGTGCTG	CAGATTTGAT	ATTTGCATTG	2760
AGGAAATATT	AATTTTCCAA	TGCACAGTTG	CCACATTTAG	TCCTGTACTG	TATGGAAACA	2820

CTGATTTTGT AAAGTTGCCT TTATTTGCTG TTAAGTGTTA ACTATGACAG ATATATTTAA 2880  
GCCTTATAAA CCAATCTTAA ACATAATAAA TCACACATTC AGTTTATAAA AAAAAAAAAA 2940  
AAAAAA 2946

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 788
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE:
  - (G) CELL TYPE: teratocarcinoma
  - (H) CELL LINE: N-tera 2D1
  - (I) ORGANELLE:
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION: N-tera 2D1 putative ATX protein sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Cys	Asp	Asn	Leu	Cys	Lys	Ser	Tyr	Thr	Ser	Cys	Cys	His	Asp	Phe	Asp
				5					10					15	
Glu	Leu	Cys	Leu	Lys	Thr	Ala	Arg	Ala	Trp	Glu	Cys	Thr	Lys	Asp	Arg
			20					25					30		
Cys	Gly	Glu	Val	Arg	Asn	Glu	Glu	Asn	Ala	Cys	His	Cys	Ser	Glu	Asp
		35				40					45				
Cys	Leu	Ala	Arg	Gly	Asp	Cys	Cys	Thr	Asn	Tyr	Gln	Val	Val	Cys	Lys
	50				55				60						
Gly	Glu	Ser	His	Trp	Val	Asp	Asp	Asp	Cys	Glu	Glu	Ile	Lys	Ala	Ala
65				70				75						80	
Glu	Cys	Leu	Gln	Val	Asp	Ser	Pro	Ser	Ile	Asn	His	Leu	Leu	Arg	Gly
			85					90					95		
Trp	Leu	Pro	Met	Thr	Ser	Tyr	Met	Lys	Gly	Ser	Lys	Val	Met	Pro	
			100				105					110			

Asn	Ile	Glu	Lys	Leu	Arg	Ser	Cys	Gly	Thr	His	Ser	Pro	Tyr	Met	Arg	
		115					120					125				
Pro	Val	Tyr	Pro	Thr	Lys	Thr	Phe	Pro	Asn	Leu	Tyr	Thr	Leu	Ala	Thr	
	130					135					140					
Gly	Leu	Tyr	Pro	Glu	Ser	His	Gly	Ile	Val	Gly	Asn	Ser	Met	Tyr	Asp	
145					150					155					160	
Pro	Val	Phe	Asp	Ala	Thr	Phe	His	Leu	Arg	Gly	Arg	Glu	Lys	Phe	Asn	
			165					170						175		
His	Arg	Trp	Trp	Ala	Gly	Gln	Pro	Leu	Trp	Ile	Thr	Ala	Thr	Lys	Gln	
			180					185					190			
Arg	Gly	Glu	Ser	Trp	Asn	Ile	Leu	Leu	Val	Cys	Cys	His	Pro	Ser	Arg	
	195						200					205				
Ala	Glu	Ile	Leu	Thr	Ile	Leu	Gln	Trp	Leu	Thr	Leu	Pro	Asp	His	Glu	
	210					215					220					
Arg	Pro	Ser	Val	Tyr	Ala	Phe	Tyr	Ser	Glu	Gln	Pro	Asp	Phe	Ser	Gly	
225					230					235					240	
His	Lys	His	Met	Pro	Phe	Gly	Pro	Glu	Met	Pro	Asn	Pro	Leu	Arg	Glu	
			245					250						255		
Met	His	Lys	Ile	Val	Gly	Gln	Leu	Met	Asp	Gly	Leu	Lys	Gln	Leu	Lys	
			260					265					270			
Leu	His	Arg	Cys	Val	Asn	Val	Ile	Phe	Val	Glu	Thr	Met	Asp	Gly	Arg	
		275					280					285				
Cys	His	Met	Tyr	Arg	Thr	Glu	Phe	Leu	Ser	Asn	Tyr	Leu	Thr	Asn	Val	
	290					295					300					
Asp	Asp	Ile	Thr	Leu	Val	Pro	Gly	Thr	Leu	Gly	Arg	Ile	Arg	Ser	Lys	
305					310					315					320	
Phe	Ser	Asn	Asn	Ala	Lys	Tyr	Asp	Pro	Lys	Ala	Ile	Ile	Ala	Asn	Leu	
			325						330					335		
Thr	Cys	Lys	Lys	Pro	Asp	Gln	His	Phe	Lys	Pro	Tyr	Leu	Lys	Gln	His	
			340					345					350			
Leu	Pro	Lys	Arg	Leu	His	Tyr	Ala	Asn	Asn	Arg	Arg	Ile	Glu	Asp	Ile	
		355					360					365				
His	Leu	Leu	Val	Glu	Arg	Arg	Trp	His	Val	Ala	Arg	Lys	Pro	Leu	Asp	
	370					375					380					
Val	Tyr	Lys	Lys	Pro	Ser	Gly	Asn	Ala	Phe	Ser	Arg	Glu	Thr	Thr	Ala	
385					390					395					400	
Phe	Asp	Asn	Lys	Val	Asn	Ser	Met	Gln	Thr	Val	Phe	Val	Gly	Tyr	Gly	
			405						410					415		
Pro	Thr	Phe	Lys	Tyr	Lys	Thr	Lys	Val	Pro	Pro	Phe	Glu	Asn	Ile	Glu	
			420					425					430			
Leu	Tyr	Asn	Val	Met	Cys	Asp	Leu	Leu	Gly	Leu	Lys	Pro	Ala	Pro	Asn	
		435					440					445				
Asn	Gly	Thr	His	Phe	Ser	Leu	Asn	His	Leu	Leu	Arg	Thr	Asn	Thr	Phe	
	450					455					460					
Arg	Pro	Thr	Met	Pro	Glu	Glu	Val	Thr	Arg	Pro	Asn	Tyr	Pro	Gly	Ile	
465					470					475					480	
Met	Tyr	Leu	Gln	Ser	Asp	Phe	Asp	Leu	Gly	Cys	Thr	Cys	Asp	Asp	Lys	
			485						490					495		
Val	Glu	Pro	Lys	Asn	Lys	Leu	Asp	Glu	Leu	Asn	Lys	Arg	Leu	His	Thr	
			500					505					510			
Lys	Gly	Ser	Thr	Glu	Glu	Arg	His	Leu	Leu	Tyr	Gly	Asp	Arg	Pro	Ala	
		515					520					525				



Val	Leu	Tyr	Arg	Thr	Arg	Tyr	Asp	Ile	Leu	Tyr	His	Thr	Asp	Phe	Glu
530						535					540				
Ser	Gly	Tyr	Ser	Glu	Ile	Phe	Leu	Met	Pro	Leu	Trp	Thr	Ser	Tyr	Thr
545					550					555					560
Val	Ser	Lys	Gln	Ala	Glu	Val	Ser	Ser	Val	Pro	Asp	His	Leu	Thr	Ser
				565					570						575
Cys	Val	Arg	Pro	Asp	Val	Arg	Val	Ser	Pro	Ser	Phe	Ser	Gln	Asn	Cys
			580					585					590		
Leu	Ala	Tyr	Lys	Asn	Asp	Lys	Gln	Met	Ser	Tyr	Gly	Gly	Leu	Gly	Pro
		595					600					605			
Pro	Tyr	Leu	Ser	Ser	Ser	Pro	Glu	Ala	Lys	Tyr	Asp	Ala	Phe	Leu	Val
	610					615					620				
Thr	Asn	Met	Val	Pro	Met	Tyr	Pro	Ala	Phe	Lys	Arg	Val	Trp	Asn	Tyr
625					630					635					640
Phe	Gln	Arg	Val	Leu	Val	Lys	Lys	Tyr	Ala	Ser	Glu	Arg	Asn	Gly	Val
				645					650					655	
Asn	Val	Ile	Ser	Gly	Pro	Ile	Phe	Asp	Tyr	Asp	Tyr	Asp	Gly	Leu	His
			660					665					670		
Asp	Thr	Glu	Asp	Lys	Ile	Lys	Gln	Tyr	Val	Glu	Gly	Ser	Ser	Ile	Pro
		675					680					685			
Val	Pro	Thr	His	Tyr	Tyr	Ser	Ile	Ile	Thr	Ser	Cys	Leu	Asp	Phe	Thr
	690					695					700				
Gln	Pro	Ala	Asp	Lys	Cys	Asp	Gly	Pro	Leu	Ser	Val	Ser	Ser	Phe	Ile
705					710					715					720
Leu	Pro	His	Arg	Pro	Asp	Asn	Glu	Glu	Ser	Cys	Asn	Ser	Ser	Glu	Asp
				725					730					735	
Glu	Ser	Lys	Trp	Val	Glu	Glu	Leu	Met	Lys	Met	His	Thr	Ala	Arg	Val
			740					745					750		
Arg	Asp	Ile	Glu	His	Leu	Thr	Ser	Leu	Asp	Phe	Phe	Arg	Lys	Thr	Ser
	755						760					765			
Arg	Ser	Tyr	Pro	Glu	Ile	Leu	Thr	Leu	Lys	Thr	Tyr	Leu	His	Thr	Tyr
	770					775					780				
Glu	Ser	Glu	Ile												
785															

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2712
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:

84572\_1

(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE: teratocarcinoma  
(H) CELL LINE: N-tera 2D1  
(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: N-tera 2D1 ATX DNA sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGTGACAACT	TGTGTAAGAG	CTATACCAGT	TGCTGCCATG	ACTTTGATGA	GCTGTGTTTG	60
AAGACAGCCC	GTGCGTGGA	GTGTACTAAG	GACAGATGTG	GGGAAGTCAG	AAATGAAGAA	120
AATGCCTGTC	ACTGCTCAGA	GGACTGCTTG	GCCAGGGGAG	ACTGCTGTAA	CAATTACCAA	180
GTGGTTTGCA	AAGGAGAGTC	GCATTGGGTT	GATGATGACT	GTGAGGAAAT	AAAGGCCGCA	240
GAATGCCTGC	AGGTTTGTTT	GCCCTCCATT	AATCATCTTC	TCCGTGGATG	GCTTCCGATG	300
ACATCATACA	TGAAGAAAGG	CAGCAAAGTC	ATGCCTAATA	TTGAAAAACT	AAGGTCTTGT	360
GGCACACACT	CTCCCTACAT	GAGGCCGGTG	TACCCAACTA	AAACCTTTTC	TAAGTTATAC	420
ACTTTGGCCA	CTGGGCTATA	TCCAGAATCA	CATGGAATTG	TTGGCAATTC	AATGTATGAT	480
CCTGTATTTG	ATGCCACTTT	TCATCTGCGA	GGGCGAGAGA	AATTTAATCA	TAGATGGTGG	540
GGAGGTCAAC	CGCTATGGAT	TACAGCCACC	AAGCAAAGGG	GTGAAAGCTG	GAACATTCTT	600
TTGGTCTGTT	GTCATCCCTC	ACGAGCGGAG	ATATTAACCA	TATTGCAGTG	GCTCACCCCTG	660
CCAGATCATG	AGAGGCCTTC	GGTCTATGCC	TTCTATTCTG	AGCAACCTGA	TTTCTCTGGA	720
CACAAACATA	TGCCTTTCGG	CCCTGAGATG	ACAAATCCTC	TGAGGGAAAT	GCACAAAATT	780
GTGGGGCAAT	TAATGGATGG	ACTGAAACAA	CTAAACTGTC	ATCGGTGTGT	CAACGTCATC	840
TTTGTCGAGA	CCATGGATGG	AAGATGTCAC	ATGTATAGAA	CTGAGTTCTT	GAGTAATTAC	900
CTAATAATG	TGGATGATAT	TACTTTAGTG	CCTGGAACTC	TAGGAAGAAAT	TCGATCCAAA	960
TTTAGCAACA	ATGCTAAATA	TCACCCCAA	GCCATTATTG	CCAATCTCAC	GTGTAAAAAA	1020
CCAGATCAGC	ACTTTAAGCC	TTACTTGAAA	CAGCACCTTC	CCAAACGTTT	GCACATGCCC	1080
AACAACAGAA	GAATTGAGGA	TATCCATTTA	TTGGTGGAAC	GCAGATGGCA	TGTTGCAAGG	1140
AAACCTTTGG	ATGTTTATAA	GAAACCATCA	GGAAATGCTT	TTTCCAGGGA	GACCACGGCA	1200
TTTGATAACA	AGGTCAACAG	CATGCAGACT	GTTTTTTGTAG	GTTATGGCCC	AACATTTAAG	1260
TACAAGACTA	AAGTDCCTCC	ATTTGAAAAC	ATTGAACTTT	AAAATGTTAT	GTGTGATCTC	1320
CTGGGATTGA	AGCCAGCTCC	TAATAATGGG	ACCCATGGAA	GTTTGAATCA	TCTCCTGCGC	1380
ACTAATACCT	TCAGGCCAAC	CATGCCAGAG	GAAGTTACCA	GACCCATTAT	TCCAGGGATT	1440
ATGTACCTTC	AGTCTGATTT	TGACCTGGGC	TGCACTTGTG	ATGATAAGGT	AGAGCCAAAG	1500
AACAAGTTGG	ATGAACTCAA	CAAACGGCTT	CATACAAAAG	GGTCTACAGA	AGAGAGACAC	1560
CTCCTCTATG	GGGATCGACC	TGCAGTGCTT	TATCGGACTA	GATATGATAT	CTTATATCAC	1620
ACTGACTTTG	AAAGTGTTTA	TAGTGAAATA	TTCTTAATGC	CACTCTGGAC	ATCATATACT	1680
GTTTCCAAAC	AGGCTGAGGT	TTCCAGCGTT	CCTGACCATC	TGACCAGTTG	CGTCCGCGCT	1740
GATGTCCTGT	TTTCTCCGAG	TTTCAGTCAG	AACTGTTTGG	CCTACAAAAA	TGATAAGCAG	1800
ATGTCCTACG	GATTCTCTTT	TCCTCCTTAT	CTGAGCTCTT	CACCAGAGGC	TAAATATGAT	1860
GCATTCTCTG	TAACCAATAT	GGTTCCAATG	TATCCTGCTT	TCAAACGGGT	CTGGAATTAT	1920
TTCCAAAGGG	TATTGGTGAA	GAAATATGCT	TCGGAAAGAA	ATGGAGTTAA	CGTGATAAGT	1980
GGACCAATCT	TCGACTATGA	CTATGATGGC	TTACATGACA	CAGAAGACAA	AATAAAACAG	2040
TACGTGGAAG	GCAGTTCCAT	TCTGTGTTCA	ACTCACTACT	ACAGCATCAT	CACCAGCTGT	2100
CTGGATTTCA	CTCAGCCTGC	CGACAAGTGT	GACGGCCCTC	TCTCTGTGTC	CTCCTTCATC	2160
CTGCCTCACC	GGCCTGACAA	CGAGGAGAGC	TGCAATAGCT	CAGAGGACGA	ATCAAAATGG	2220

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GTAGAAGAAC TCATGAAGAT GCACACAGCT AGGGTGCGTG ACATTGAACA TCTCACCAGC 2280
CTGGACTTCT TCCGAAAGAC CAGCCGCAGC TACCCAGAAA TCCTGACACT CAAGACATAC 2340
CTGCATACAT ATGAGAGCGA GATTTAACTT TCTGAGCATC TGCAGTACAG TCTTATCAAC 2400
TGGTTGTATA TTTTATATATT GTTTTGTAT TTATTAATTT GAAACCAGGA CATTAAAAAT 2460
GTTAGTATTT TAATCCTGTA CCAAATCTGA CATATTATGC CTGAATGACT CCACTGTTTT 2520
TCTCTAATGC TTGATTTAGG TAGCCTTGTG TTCTGAGTAG AGCTTGTAAT AAATACTGCA 2580
GCTTGAGTTT TTAGTGGAAG CTTCTAAATG GTGCTGCAGA TTTGATATTT GCATTGAGGA 2640
AATATTAATT TTCCAATGCA CAGTTGCCAC ATTTAGTCCT GTACTGTATG GAAACACTGA 2700
TTTTGTAAAG TT 2712
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(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE: Liver
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: putative autotaxin protein  
sequence from human liver

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

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Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Asp Ile Ser Leu Phe
                    5              10
Thr Phe Ala Val Gly Val Asn Ile Cys Leu Gly Phe Thr Ala His Arg
                    20              25              30
Ile Lys Arg Ala Glu Gly Trp Glu Gly Pro Pro Thr Val Leu Ser
                    35              40              45
Asp Ser Pro Trp Thr Asn Ile Ser Gly Ser Cys Lys Gly Arg Cys Phe
                    50              55              60
```

Glu	Leu	Gln	Glu	Ala	Gly	Pro	Pro	Asp	Cys	Arg	Cys	Asp	Asn	Leu	Cys
65					70					75					80
Lys	Ser	Tyr	Thr	Ser	Cys	Cys	His	Asp	Phe	Asp	Glu	Leu	Cys	Leu	Lys
				85					90					95	
Thr	Ala	Arg	Ala	Trp	Glu	Cys	Thr	Lys	Asp	Arg	Cys	Gly	Glu	Val	Arg
			100					105					110		
Asn	Glu	Glu	Asn	Ala	Cys	His	Cys	Ser	Glu	Asp	Cys	Leu	Ala	Arg	Gly
		115					120					125			
Asp	Cys	Cys	Thr	Asn	Tyr	Gln	Val	Val	Cys	Lys	Gly	Glu	Ser	His	Trp
	130					135					140				
Val	Asp	Asp	Asp	Cys	Glu	Glu	Ile	Lys	Ala	Ala	Glu	Cys	Leu	Gln	Val
145					150					155					160
Cys	Ser	Pro	Ser	Ile	Asn	His	Leu	Leu	Arg	Gly	Trp	Leu	Pro	Met	Thr
				165					170					175	
Ser	Tyr	Met	Lys	Lys	Gly	Ser	Lys	Val	Met	Pro	Asn	Ile	Glu	Lys	Leu
			180					185					190		
Arg	Ser	Cys	Gly	Thr	His	Ser	Pro	Tyr	Met	Arg	Pro	Val	Tyr	Pro	Thr
		195					200					205			
Lys	Thr	Phe	Pro	Asn	Leu	Tyr	Thr	Leu	Ala	Thr	Gly	Leu	Tyr	Pro	Glu
	210					215					220				
Ser	His	Gly	Ile	Val	Gly	Asn	Ser	Met	Tyr	Asp	Pro	Val	Phe	Asp	Ala
225					230					235					240
Thr	Phe	His	Leu	Arg	Gly	Arg	Glu	Lys	Phe	Asn	His	Arg	Trp	Trp	Gly
				245					250					255	
Gly	Gln	Pro	Leu	Trp	Ile	Thr	Ala	Thr	Lys	Gln	Arg	Gly	Glu	Ser	Trp
			260					265					270		
Asn	Ile	Leu	Leu	Val	Cys	Cys	His	Pro	Ser	Arg	Ala	Glu	Ile	Leu	Thr
		275					280					285			
Ile	Leu	Gln	Trp	Leu	Thr	Leu	Pro	Asp	His	Glu	Arg	Pro	Ser	Val	Tyr
	290					295					300				
Ala	Phe	Tyr	Ser	Glu	Gln	Pro	Asp	Phe	Ser	Gly	His	Lys	His	Met	Pro
305					310					315					320
Phe	Gly	Pro	Glu	Met	Thr	Asn	Pro	Leu	Arg	Glu	Met	His	Lys	Ile	Val
				325					330					335	
Gly	Gln	Leu	Met	Asp	Gly	Leu	Lys	Gln	Leu	Lys	Leu	His	Arg	Cys	Val
			340					345					350		
Asn	Val	Ile	Phe	Val	Glu	Thr	Met	Asp	Gly	Arg	Cys	His	Met	Tyr	Arg
		355					360					365			
Thr	Glu	Phe	Leu	Ser	Asn	Tyr	Leu	Thr	Asn	Val	Asp	Asp	Ile	Thr	Leu
	370					375					380				
Val	Pro	Gly	Thr	Leu	Gly	Arg	Ile	Arg	Ser	Lys	Phe	Ser	Asn	Asn	Ala
385					390					395					400
Lys	Tyr	Asp	Pro	Lys	Ala	Ile	Ile	Ala	Asn	Leu	Thr	Cys	Lys	Lys	Pro
				405					410					415	
Asp	Gln	His	Phe	Lys	Pro	Tyr	Leu	Lys	Gln	His	Leu	Pro	Lys	Arg	Leu
			420					425					430		
His	Tyr	Ala	Asn	Asn	Arg	Arg	Ile	Glu	Asp	Ile	His	Leu	Leu	Val	Glu
		435					440					445			
Arg	Arg	Trp	His	Val	Ala	Arg	Lys	Pro	Leu	Asp	Val	Tyr	Lys	Lys	Pro
	450					455					460				
Ser	Gly	Asn	Ala	Phe	Ser	Arg	Glu	Thr	Thr	Ala	Phe	Asp	Asn	Lys	Val
465					470					475					480

Asn	Ser	Met	Gln	Thr	Val	Phe	Val	Gly	Tyr	Gly	Pro	Thr	Phe	Lys	Tyr
				485					490					495	
Lys	Thr	Lys	Val	Pro	Pro	Phe	Glu	Asn	Ile	Glu	Leu	Tyr	Asn	Val	Met
			500					505					510		
Cys	Asp	Leu	Leu	Gly	Leu	Lys	Pro	Ala	Pro	Asn	Asn	Gly	Thr	His	Gly
		515					520					525			
Ser	Leu	Asn	His	Leu	Leu	Arg	Thr	Asn	Thr	Phe	Arg	Pro	Thr	Met	Pro
	530					535					540				
Glu	Glu	Val	Thr	Arg	Pro	Asn	Tyr	Pro	Gly	Ile	Met	Tyr	Leu	Gln	Ser
545					550					555					560
Asp	Phe	Asp	Leu	Gly	Cys	Thr	Cys	Asp	Asp	Lys	Val	Glu	Pro	Lys	Asn
				565					570					575	
Lys	Leu	Asp	Glu	Leu	Asn	Lys	Arg	Leu	His	Thr	Lys	Gly	Ser	Thr	Glu
			580					585					590		
Glu	Arg	His	Leu	Leu	Tyr	Gly	Asp	Arg	Pro	Ala	Val	Leu	Tyr	Arg	Thr
		595					600					605			
Arg	Tyr	Asp	Ile	Leu	Tyr	His	Thr	Asp	Phe	Glu	Ser	Gly	Tyr	Ser	Glu
	610					615					620				
Ile	Phe	Leu	Met	Pro	Leu	Trp	Thr	Ser	Tyr	Thr	Val	Ser	Lys	Gln	Ala
625					630					635					640
Glu	Val	Ser	Ser	Val	Pro	Asp	His	Leu	Thr	Ser	Cys	Val	Arg	Pro	Asp
				645					650					655	
Val	Arg	Val	Ser	Pro	Ser	Phe	Ser	Gln	Asn	Cys	Leu	Ala	Tyr	Lys	Asn
			660					665					670		
Asp	Lys	Gln	Met	Ser	Tyr	Gly	Phe	Leu	Phe	Pro	Pro	Tyr	Leu	Ser	Ser
		675					680					685			
Ser	Pro	Glu	Ala	Lys	Tyr	Asp	Ala	Phe	Leu	Val	Thr	Asn	Met	Val	Pro
	690					695					700				
Met	Tyr	Pro	Ala	Phe	Lys	Arg	Val	Trp	Asn	Tyr	Phe	Gln	Arg	Val	Leu
705					710					715					720
Val	Lys	Lys	Tyr	Ala	Ser	Glu	Arg	Asn	Gly	Val	Asn	Val	Ile	Ser	Gly
				725					730					735	
Pro	Ile	Phe	Asp	Tyr	Asp	Tyr	Asp	Gly	Leu	His	Asp	Thr	Glu	Asp	Lys
			740					745					750		
Ile	Lys	Gln	Tyr	Val	Glu	Gly	Ser	Ser	Ile	Pro	Val	Pro	Thr	His	Tyr
		755					760					765			
Tyr	Ser	Ile	Ile	Thr	Ser	Cys	Leu	Asp	Phe	Thr	Gln	Pro	Ala	Asp	Lys
	770					775					780				
Cys	Asp	Gly	Pro	Leu	Ser	Val	Ser	Ser	Phe	Ile	Leu	Pro	His	Arg	Pro
785					790					795					800
Asp	Asn	Glu	Glu	Ser	Cys	Asn	Ser	Ser	Glu	Asp	Glu	Ser	Lys	Trp	Val
				805					810					815	
Glu	Glu	Leu	Met	Lys	Met	His	Thr	Ala	Arg	Val	Arg	Asp	Ile	Glu	His
			820					825					830		
Leu	Thr	Ser	Leu	Asp	Phe	Phe	Arg	Lys	Thr	Ser	Arg	Ser	Tyr	Pro	Glu
		835					840					845			
Ile	Leu	Thr	Leu	Lys	Thr	Tyr	Leu	His	Thr	Tyr	Glu	Ser	Glu	Ile	Xaa
	850					855					860				
Leu	Ser	Glu	His	Leu	Gln	Tyr	Ser	Leu	Ile	Asn	Trp	Leu	Tyr	Ile	Phe
865					870					875					880
Ile	Leu	Phe	Leu	Tyr	Leu	Leu	Ile	Xaa	Asn	Gln	Asp	Ile	Lys	Asn	Val
				885					890					895	

Ser	Ile	Leu	Ile	Leu	Tyr	Gln	Ile	Xaa	His	Ile	Met	Pro	Glu	Xaa	Leu
			900					905					910		
His	Cys	Phe	Ser	Leu	Met	Leu	Asp	Leu	Gly	Ser	Leu	Val	Phe	Xaa	Val
		915					920					925			
Glu	Leu	Val	Ile	Asn	Thr	Ala	Ala	Xaa	Val	Phe	Ser	Gly	Ser	Phe	Xaa
		930				935					940				
Met	Val	Leu	Gln	Ile	Xaa	Tyr	Leu	His	Xaa	Gly	Asn	Ile	Asn	Phe	Pro
945					950					955					960
Met	His	Ser	Cys	His	Ile	Xaa	Ser	Cys	Thr	Val	Trp	Lys	His	Xaa	Phe
				965					970					975	
Cys	Lys	Val													

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: ATX-204
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met His Thr Ala Arg Val Arg Asp  
5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: ATX-205
- (B) LOCATION:

- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Phe Ser Asn Asn Ala Lys Tyr Asp  
5

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7
  - (B) TYPE: amino acids
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: Peptide
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
  - (A) NAME/KEY: ATX-209
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Val Met Pro Asn Ile Glu Lys  
5

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8
  - (B) TYPE: amino acids
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: Peptide
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
  - (A) NAME/KEY: ATX-210
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr Ala Arg Gly Trp Glu Cys Thr  
5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: ATX-212
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Xaa Asp Ser Pro Trp Thr Xaa Ile Ser Gly Ser  
5 10

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: ATX-214
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

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Leu Arg Ser Cys Gly Thr His Ser Pro Tyr Met  
5 10

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: Peptide
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
  - (A) NAME/KEY: ATX-215/34A
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Thr Tyr Leu His Thr Tyr Glu Ser  
5

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13
  - (B) TYPE: amino acids
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: Peptide
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ala Ile Ile Ala Asn Leu Thr Cys Lys Lys Pro Asp Gln  
5 10

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: ATX-216
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ile Val Gly Gln Leu Met Asp Gly  
5

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: ATX-218/44
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Thr Ser Arg Ser Tyr Pro Glu Ile Leu  
5

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: ATX-223B/24
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Gln Ala Glu Val Ser Ser Val Pro Asp  
5

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: ATX-224
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Arg Cys Phe Glu Leu Gln Glu Ala Gly Pro Pro Asp Asp Cys  
5 10

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: ATX-229
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Ser Tyr Thr Ser Cys Cys His Asp Phe Asp Glu Leu  
5 10

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: ATX-224/53
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro Tyr Leu Ser Ser Ser Pro  
5 10 15

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE: Liver
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: 5' end of human liver ATX gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATGGCAAGGA GGAGCTCGTT CCAGTCGTGT CAAGATATAT CCCTGTTCAC TTTTGCCGTT 60  
GGAGTCAATA TCTGCTTAGG ATTCAGTCA CATCGAATTA AGAGAGCAGA AGGATGG 117

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: Peptide

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(iii) HYPOTHETICAL: No

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE: Liver
- (G) CELL TYPE:
- (H) CELL LINE:
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: N-terminal region including transmembrane domain of liver ATX protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Ala	Arg	Arg	Ser	Ser	Phe	Gln	Ser	Cys	Gln	Asp	Ile	Ser	Leu	Phe
				5					10					15	
Thr	Phe	Ala	Val	Gly	Val	Asn	Ile	Cys	Leu	Gly	Phe	Thr	Ala	His	Arg
			20					25					30		
Ile	Lys	Arg	Ala	Glu	Gly	Trp									
			35												